

09/936,146.

=> s (oligo? or nucleo?) (5a) trans splic? (10a) 3(2a) exon?
L30 6 (OLIGO? OR NUCLEO?) (5A) TRANS SPLIC? (10A) 3(2A) EXON?

=> s 130 not 129
L31 6 L30 NOT L29

=> dup rem 131
PROCESSING COMPLETED FOR L31
L32 4 DUP REM L31 (2 DUPLICATES REMOVED)

=> d 132 1-4 bib abs

L32 ANSWER 1 OF 4 USPATFULL on STN
AN 2004:221289 USPATFULL
TI Alteration of sequence of a target molecule
IN Sullenger, Bruce, Westminster, CO, UNITED STATES
Cech, Thomas, Boulder, CO, UNITED STATES
PI US 2004171058 A1 20040902
AI US 2004-799535 A1 20040312 (10)
RLI Continuation of Ser. No. US 1998-165514, filed on 2 Oct 1998, ABANDONED
Continuation of Ser. No. US 1997-786753, filed on 24 Jan 1997, GRANTED,
Pat. No. US 5869254 Continuation of Ser. No. US 1993-152450, filed on 12
Nov 1993, GRANTED, Pat. No. US 5667969
DT Utility
FS APPLICATION
LREP Patrick G. Gattari, McDonnell Boehnen Hulbert & Berghoff, 32nd Floor,
300 S. Wacker Drive, Chicago, IL, 60606
CLMN Number of Claims: 12
ECL Exemplary Claim: 1
DRWN 8 Drawing Page(s)
LN.CNT 993
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Method for splicing a target nucleic acid molecule with a separate
nucleic acid molecule. Such splicing generally causes production of a
chimeric protein with advantageous features over that protein naturally
produced from the target nucleic acid prior to splicing. The method
includes contacting the target nucleic acid molecule with a catalytic
nucleic acid molecule including the separate nucleic acid molecule. Such
contacting is performed under conditions in which at least a portion of
the separate nucleic acid molecule is spliced with at least a portion of
the target nucleic acid molecule to form a chimeric nucleic acid
molecule. In this method, the catalytic nucleic molecule is chosen so
that it is not naturally associated with the separate nucleic acid
molecule.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L32 ANSWER 2 OF 4 USPATFULL on STN
AN 1999:18925 USPATFULL
TI Alteration of sequence of a target molecule by ribozyme catalyzed
trans-splicing
IN Sullenger, Bruce A., Westminster, CO, United States
Cech, Thomas R., Boulder, CO, United States
PA University Research Corporation, Boulder, CO, United States (U.S.
corporation)
PI US 5869254 19990209
AI US 1997-786753 19970124 (8)
RLI Continuation of Ser. No. US 1993-152450, filed on 12 Nov 1993, now
patented, Pat. No. US 5667969
DT Utility
FS Granted

EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Fredman, Jeffrey
LREP Lyon & Lyon LLP
CLMN Number of Claims: 6
ECL Exemplary Claim: 2
DRWN 12 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 977

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Method for splicing a target nucleic acid molecule with a separate nucleic acid molecule. Such splicing generally causes production of a chimeric protein with advantageous features over that protein naturally produced from the target nucleic acid prior to splicing. The method includes contacting the target nucleic acid molecule with a catalytic nucleic acid molecule including the separate nucleic acid molecule. Such contacting is performed under conditions in which at least a portion of the separate nucleic acid molecule is spliced with at least a portion of the target nucleic acid molecule to form a chimeric nucleic acid molecule. In this method, the catalytic nucleic molecule is chosen so that it is not naturally associated with the separate nucleic acid molecule.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L32 ANSWER 3 OF 4 USPATFULL on STN

AN 97:83798 USPATFULL

TI Alteration of sequence of a deleterious target molecule by ribozyme catalyzed trans-splicing

IN Sullenger, Bruce A., Westminster, CO, United States

Cech, Thomas R., Boulder, CO, United States

PA University Research Corporation, Boulder, CO, United States (U.S. corporation)

PI US 5667969 19970916

AI US 1993-152450 19931112 (8)

DT Utility

FS Granted

EXNAM Primary Examiner: Zitomer, Stephanie W.; Assistant Examiner: Fredman, Jeffrey

LREP Lyon & Lyon

CLMN Number of Claims: 7

ECL Exemplary Claim: 1

DRWN 8 Drawing Figure(s); 10 Drawing Page(s)

LN.CNT 1006

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Method for splicing a target nucleic acid molecule with a separate nucleic acid molecule. Such splicing generally causes production of a chimeric protein with advantageous features over that protein naturally produced from the target nucleic acid prior to splicing. The method includes contacting the target nucleic acid molecule with a catalytic nucleic acid molecule including the separate nucleic acid molecule. Such contacting is performed under conditions in which at least a portion of the separate nucleic acid molecule is spliced with at least a portion of the target nucleic acid molecule to form a chimeric nucleic acid molecule. In this method, the catalytic nucleic molecule is chosen so that it is not naturally associated with the separate nucleic acid molecule.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L32 ANSWER 4 OF 4 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN
DUPLICATE 1

AN 1993:73882 BIOSIS

DN PREV199395038382

TI Analysis of the Caenorhabditis elegans axonal guidance and outgrowth gene

unc-33.

AU Li, Wei; Herman, Robert K.; Shaw, Jocelyn E.
CS Dep. Genetics Cell Biol., Univ. Minn., St. Paul, Minnesota 55108, USA
SO Genetics, (1992) Vol. 132, No. 3, pp. 675-689.
CODEN: GENTAE. ISSN: 0016-6731.

DT Article
LA English
ED Entered STN: 26 Jan 1993
Last Updated on STN: 26 Jan 1993

AB Mutations in the unc-33 gene of the nematode *Caenorhabditis elegans* lead to severely uncoordinated movement, abnormalities in the guidance and outgrowth of the axons of many neurons, and a superabundance of microtubules in neuronal processes. We have cloned unc-33 by tagging the gene with the transposable element Tc4. Three unc-33 messages, which are transcribed from a genomic region of at least 10 kb, were identified and characterized. The three messages have common 3' ends and identical reading frames. The largest (3.8-kb) message consists of the 22-**nucleotide trans-spliced** leader SL1 and 10 **exons** (I-X); the intermediate-size (3.3-kb) message begins with SL1 spliced to the 5' end of exon V and includes exons V-X; and the smallest (2.8-kb) message begins within exon VII and also includes exons VIII-X. A gamma-ray-induced deletion mutation situated within exon VIII reduces the sizes of all three messages by 0.5 kb. The three putative polypeptides encoded by the three messages overlap in C-terminal sequence but differ by the positions at which their N termini begin; none has significant similarity to any other known protein. A Tc4 insertion in exon VII leads to alterations in splicing that result in three approximately wild-type-size messages: the Tc4 sequence and 28 additional nucleotides are spliced out of the two larger messages; the Tc4 sequence is trans-spliced off the smallest message such that SL1 is added 13 nucleotides upstream of the normal 5' end of the smallest message.